Statistical and Graph Theoretical Approaches to Semantic Tagging of Unstructured Text for the BKC

DHS Advanced Scientific Computing Program

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Motivation and Goals

- Over 100 data sources have been initially identified for inclusion in the BKC; most of them contain rich information in the form of free text

- The amount of relevant information is increasing daily making manual reading and curation infeasible

- **Our goals:**

  – Provide methods for automatic extraction and semantic tagging of important information from free text to make it accessible through the BKC semantic graph

  – Facilitate efficient querying over the semantic graph
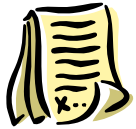
System Overview

Documents

Analyst

OIE Disease Reports

CDC Reports

ProMed Mail

Thesaurus   **Training Data**

Concepts Dictionary

Pre-processor
- Sentence Splitting
- Tokenize Sentence
- Syntax Tagging
- Anaphora Resolution
- Stop words removing
- Stemming
- N-gram generation

Algorithmic Core
- Keyphrases extraction
- Keyphrases weighting
- Named entity recognition
- Efficient graph algorithms
- Relationships extraction

Threat
Gene   Protein
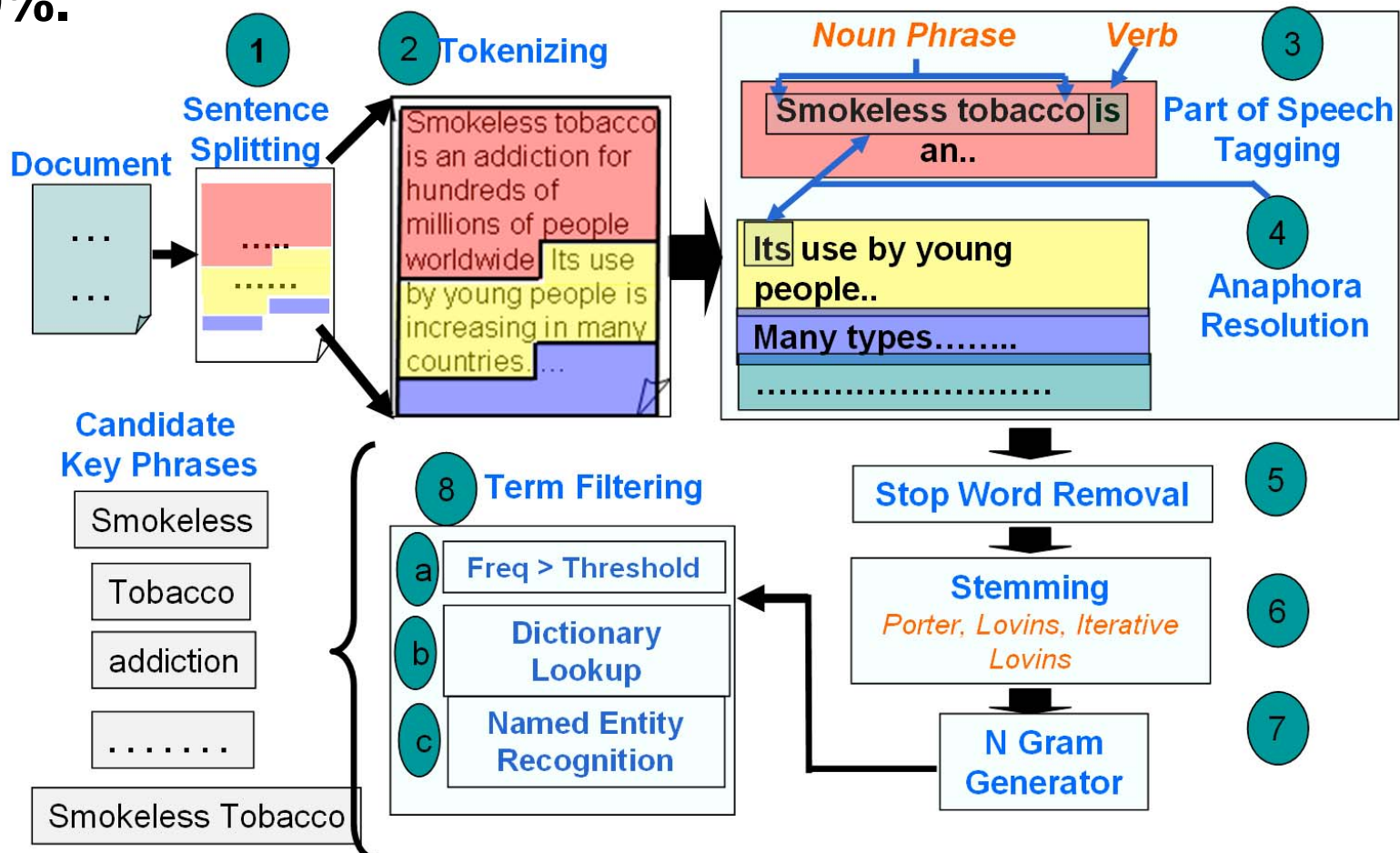Host   Signature
Fubar   Pathogen

Location
(new concept)

Foot and Mouth Disease
A virus of the family **Picornaviridae, genus** *Aphthovirus*. Seven immunologically distinct serotypes: A, O, C, SAT1, SAT2, SAT3, Asia1.
Hosts: **Bovidae (cattle, zebus, domestic buffaloes, yaks), sheep, goats**, swine, all wild ruminants and suidae. **Camelidae (camels, dromedaries, llamas, vicunas**) have low susceptibility. FMD is endemic in parts of **Asia, Africa, the Middle East and South America** (sporadic outbreaks in free areas)
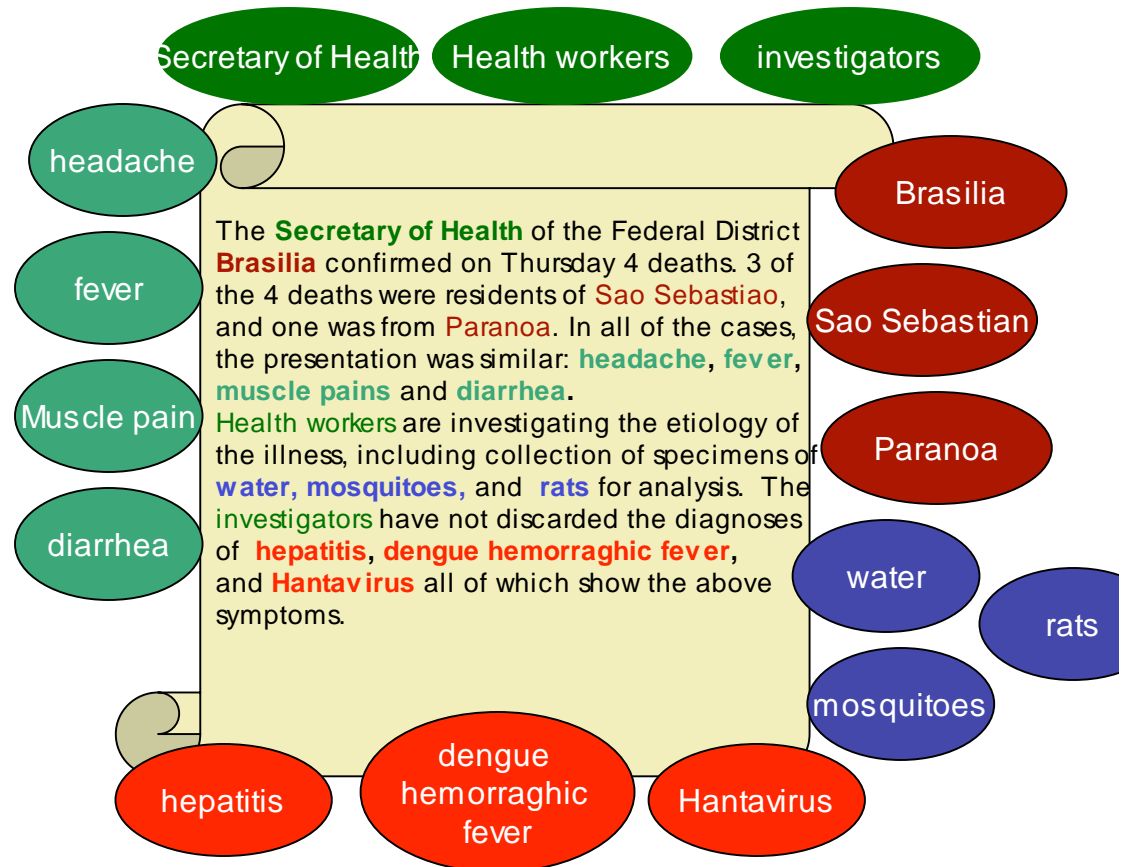
Intelligent Text Preprocessing within BKC

Text preprocessing is critical since it can improve the performance of text analysis algorithms by 15-20%.

Keyphrases Extraction and Weighting

- Keyphrases extraction is often the first step towards extracting information from free text documents.

- Keyphrases provide a reasonable understanding of the document content.

- Appropriate weights give the relevance of a document to a particular topic.
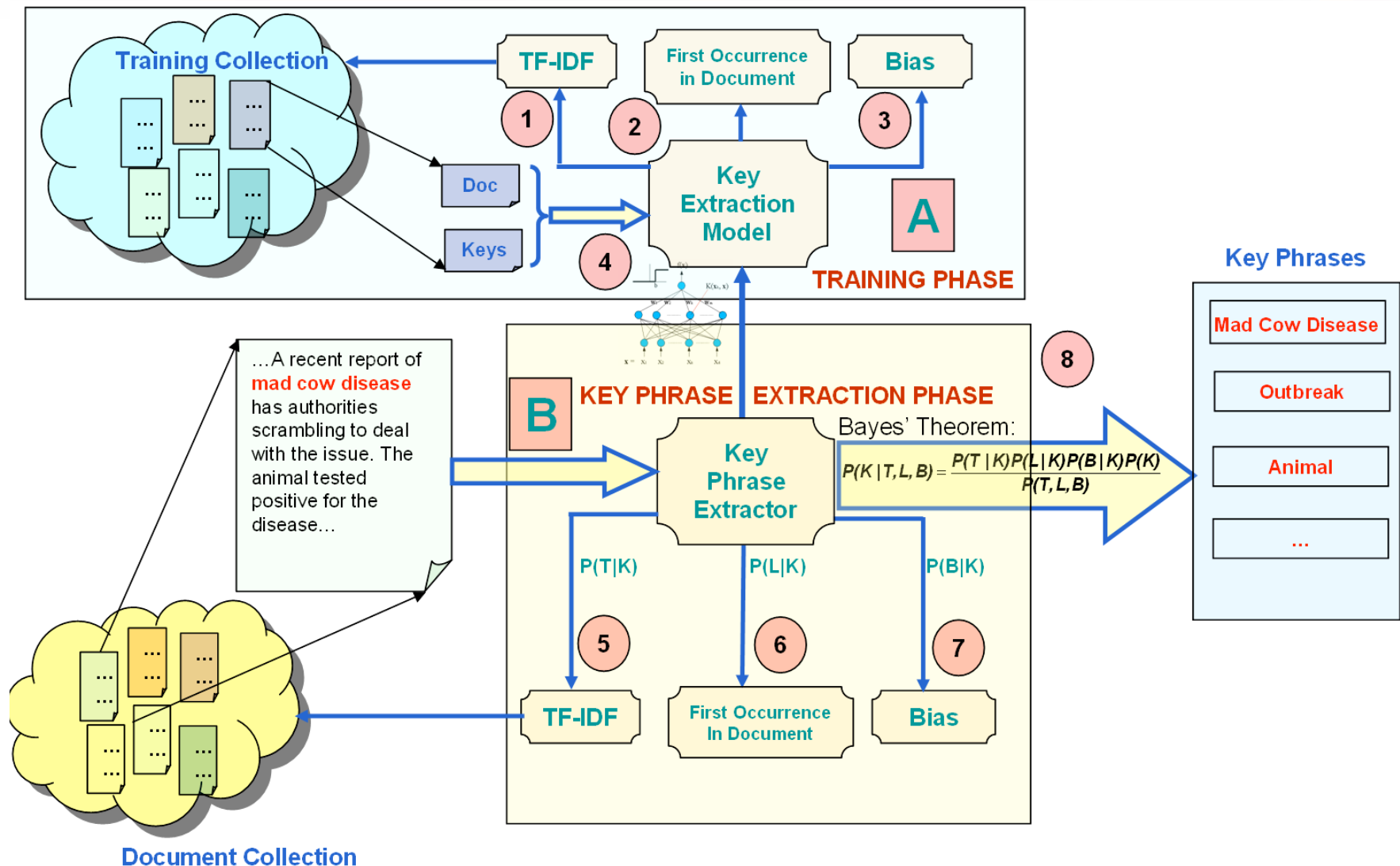
Secretary of Health   Health workers   investigators

headache

Brasilia

fever

Sao Sebastian

Muscle pain

Paranoa

diarrhea

water

rats

mosquitoes

The **Secretary of Health** of the Federal District **Brasilia** confirmed on Thursday 4 deaths. 3 of the 4 deaths were residents of Sao Sebastiao, and one was from Paranoa. In all of the cases, the presentation was similar: **headache**, **fever**, **muscle pains** and **diarrhea**.
Health workers are investigating the etiology of the illness, including collection of specimens of **water, mosquitoes,** and **rats** for analysis. The investigators have not discarded the diagnoses of **hepatitis**, **dengue hemorraghic fever**, and **Hantavirus** all of which show the above symptoms.

hepatitis   dengue hemorraghic fever   Hantavirus

Approaches to Keyphrases Extraction –
Corpus-Dependent and Corpus-Independent Methods

- A **corpus dependent** approach can be very useful when documents come from the *same source* and usually pertain to *related topics*.
  - We developed a Naïve Bayesian classifier method for situations that allow a corpus-dependent approach.
  - Utilizes **domain-specific knowledge** relevant to BKC as a basis for the bias in the Corpus Dependent Method.
  - Provides marked improvement in the observed keyphrase extraction.
  - Allows identification of documents relevant to BKC without forcing inclusion of documents simply because they contain a related term.

- A **corpus independent** approach can be very useful if the source of the documents is not very consistent and the documents could belong to *a variety of domains*.
  - We developed a term co-occurrence based algorithm for situations that call for a single-document method.

Corpus-Dependent Keyphrase Extraction

Corpus-Independent Keyphrase Extraction

$$\chi'^2(w) = \sum_{c \in G} \left\{ \frac{(freq(w,c) - n_w p_c)^2}{n_w p_c} \right\} - \max_{c \in G} \left\{ \left(\frac{(freq(w,c) - n_w p_c)^2}{n_w p_c} \right) \right\}$$

1 Top 30% words filtered by TF method

Term Clustering

2

3

Co-occurrence Distribution Significance Score (X^2)

Smokeless tobacco is an addiction for hundreds of millions of people worldwide. Use by young people is increasing in many countries. Many types of smokeless tobacco are marketed for oral or nasal use. All contain nicotine and nitrosamines. DNA and haemoglobin adducts are commonly detected in tobacco users

Tobacco users are exposed to differing levels of nitrosamines. These are formed mainly by nitrosation of nicotine and other tobacco alkaloids during the curing and processing of tobacco, and additional amounts are formed during smoking......

Frequent terms

All terms	tobacco	use	addict	…	X^2
tobacco	-	6	3	11	132
use	6	-		7	30
nicotine	8	5	5	2	342
expose	5	7	1	4	23
…	…	…	…	…	…
direct expose	2	5	1	7	258
smokeless tobacco	9	4	2	0	545

4

N-Gram collapsing

Co-occurrence matrix

Terms Clustering – Similarity Measures

Distribution-based Similarity

- Two terms are considered to be similar if they have similar co-occurrence distribution of co-occurrence with all the other terms.

- **Jensen-Shannon divergence value** of two terms indicates the distribution similarity.

$$J(w_1, w_2) = \log_2 2 + 1/2 \sum_{w` \in G} \left\{ h(P(w`|w_1) + P(w`|w_2)) - h(P(w`|w_1)) - h(P(w`|w_2)) \right\}$$

Where

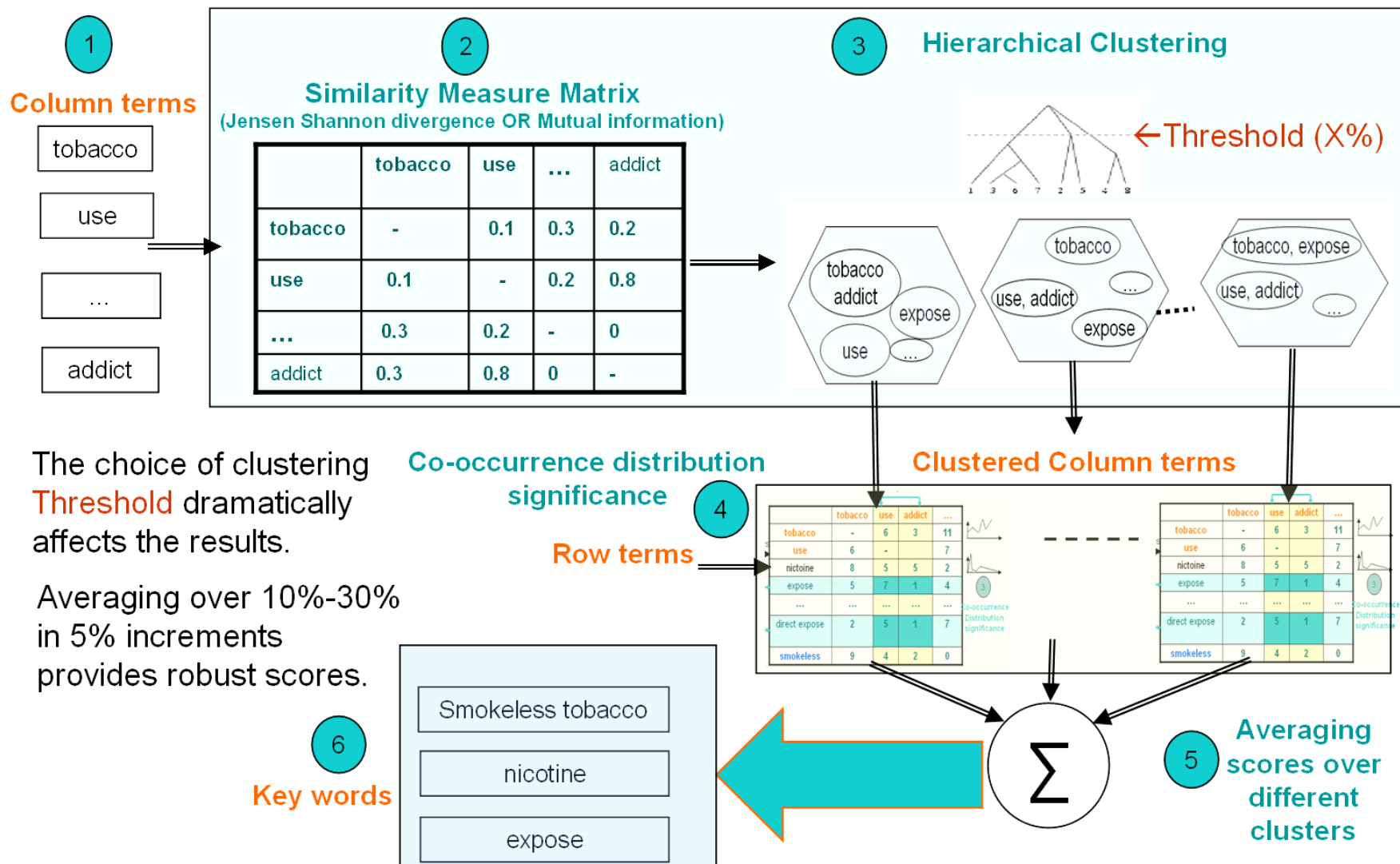$$h(x) = -x \log x, \quad P(w`|w1) = freq(w`, w1) / freq(w1)$$

Pair-wise Similarity

- Two terms are assumed similar if they co-occur frequently.
- Pair-wise similarity is measured by **mutual information**

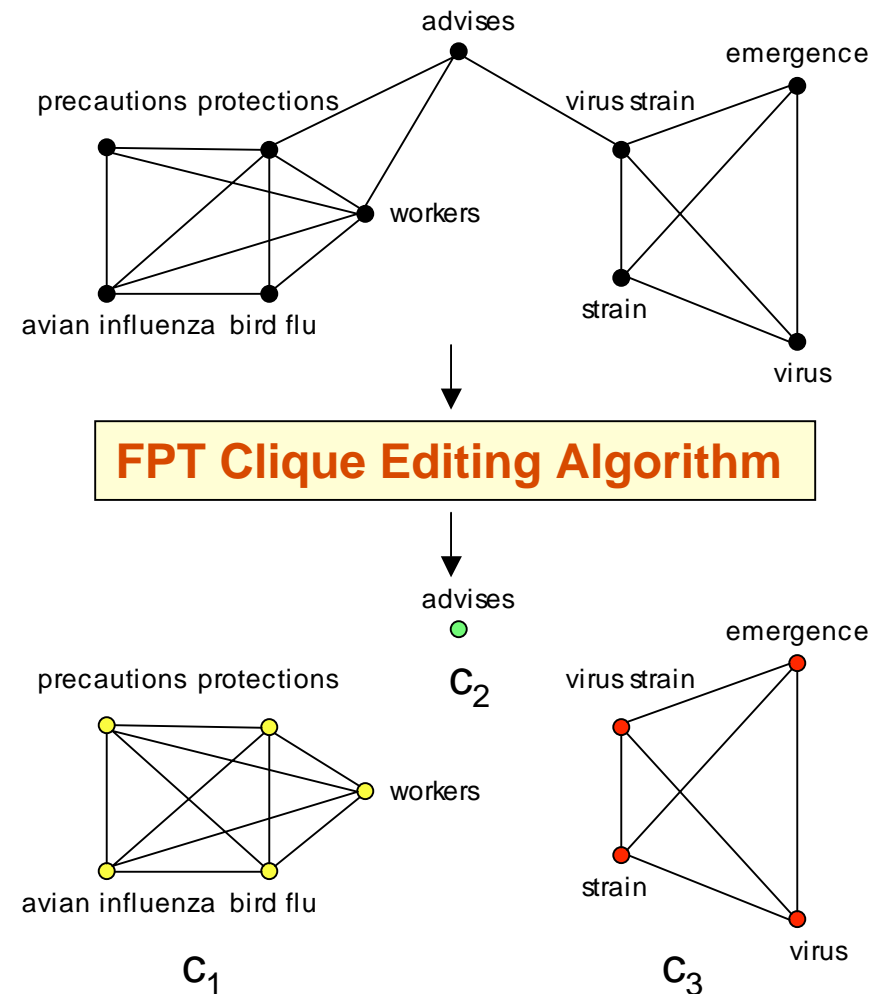$$M(w_1, w_2) = \log \frac{P(w_1, w_2)}{P(w_1)\, P(w_2)}$$

Terms Clustering
Averaging hierarchical model based clustering scores

1 Column terms

- tobacco
- use
- ...
- addict

2 Similarity Measure Matrix
(Jensen Shannon divergence OR Mutual information)

	tobacco	use	...	addict
tobacco	-	0.1	0.3	0.2
use	0.1	-	0.2	0.8
...	0.3	0.2	-	0
addict	0.3	0.8	0	-

3 Hierarchical Clustering

←Threshold (X%)

The choice of clustering Threshold dramatically affects the results.

Averaging over 10%-30% in 5% increments provides robust scores.

Co-occurrence distribution significance

4 Row terms

Clustered Column terms

6 Key words

- Smokeless tobacco
- nicotine
- expose

Σ

5 Averaging scores over different clusters

Clique-based Term Clustering

- The choice of clustering Threshold dramatically affects the results. Averaging partially solves this problem.

- Still, hierarchical clustering assigns each term to a single cluster – no overlaps. However, latent semantic meaning of terms should allow terms belong to multiple clusters.

- We developed a form of clique-based clustering based on our efficient FPT clique editing algorithm.

- Benefits:
  – No need to *a priori* specify the number of clusters (reducing the error due to Thresholding)
  – Overall quality of clusters is better or comparable with the averaging method
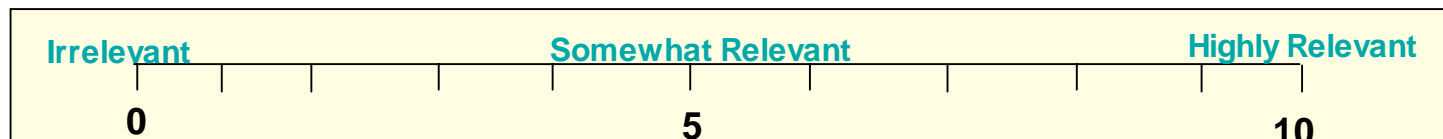 – Comparable computational time on small/medium documents with the averaging method

FPT Clique Editing Algorithm

Evaluation of Keyphrases Extraction Methods

Document Collection:

Document Set	No of Documents
Aliweb	6
CSTR	12
Journal	6

Evaluation Method:

Irrelevant	Somewhat Relevant	Highly Relevant
0	5	10

- **Top 15** keyphrases extracted by each algorithm were selected for evaluation

- **Individual Keyphrase quality** – Each keyphrase was scored according to its relevance to the document

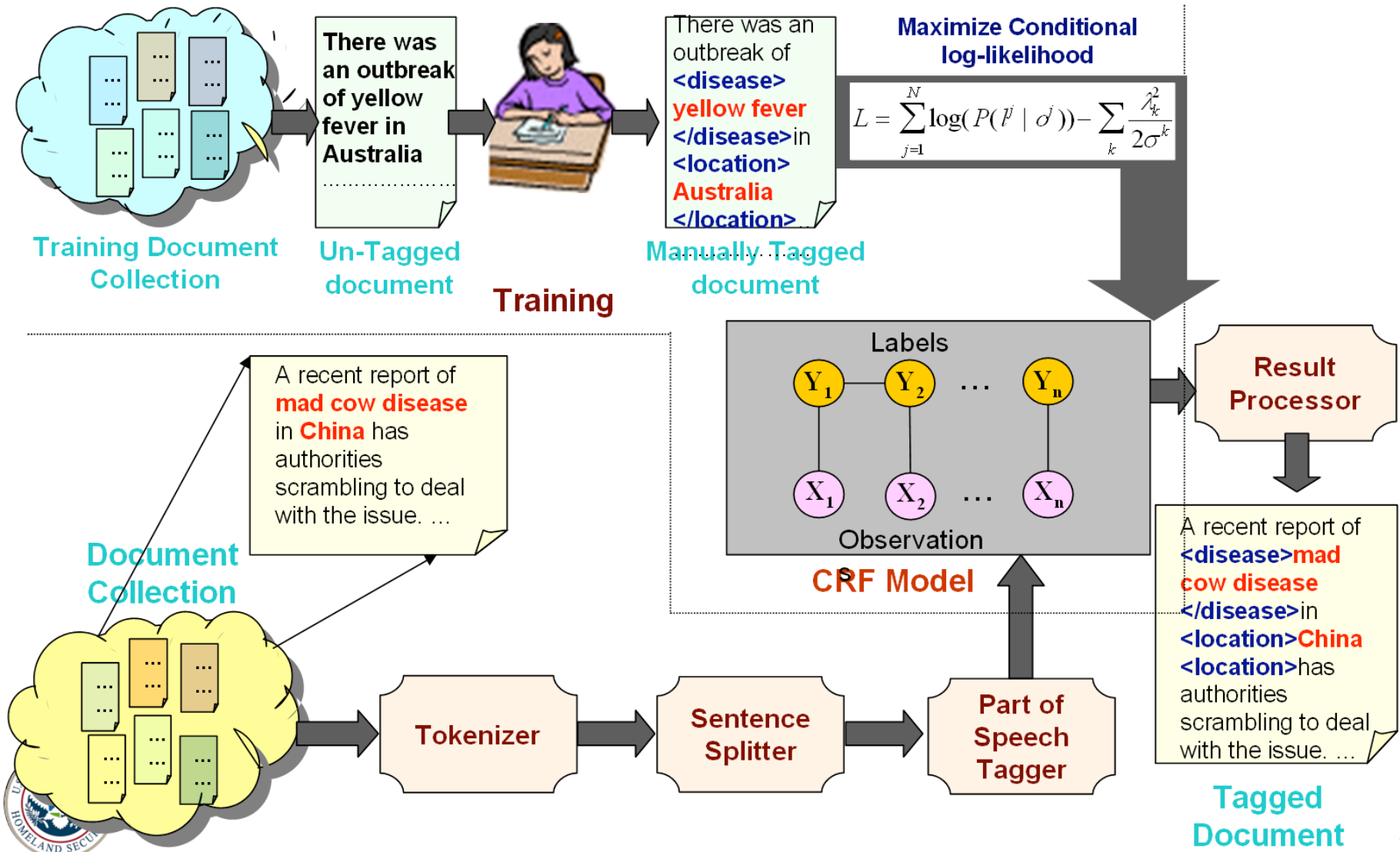- **Topic Coverage** – Entire keyphrase set was evaluated for coverage of topic(s) in the document

Results – *Manual* Evaluation of Key Phrases
Based on independent evaluation by 6 users

Algorithm	Keyphrase Quality			Topic Coverage		
	Average	Std Dev.	Avg. Rank	Average	Std Dev.	Avg. Rank
Author Assigned	5.8	1.7	9	5.9	1.2	6.4
Corpus Dependent (with Domain Bayes)	4.9	1.2	8	6.6	0.6	8.4
Corpus Dependent (no Domain Bayes)	4.7	1.3	6.8	6.4	0.7	7.4
TF-IDF	4.6	1.3	5.9	5.9	1.2	6.4
TF	4.1	1.5	4.4	5.2	1.1	4.2
Corpus Independent	4.5	1.4	5.8	5.8	1.3	6.4

- Corpus Independent algorithm compares very well with Corpus Dependent ones. The results are very much identical to TF-IDF method.
- Corpus Independent algorithm could extract more human readable phrases than TF or TF-IDF method.
- Corpus Independent method outperforms TF method that is also a corpus independent method in all respects.

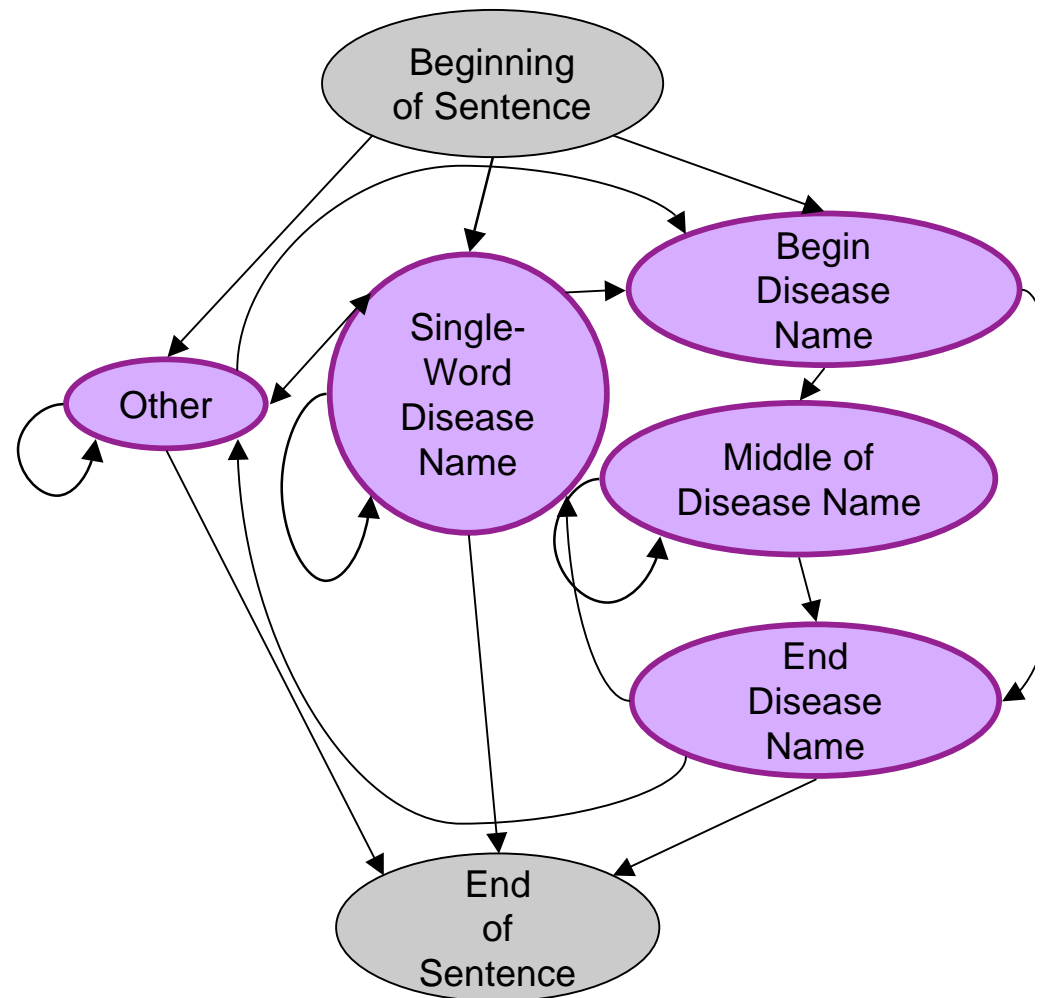# Named Entity Recognition Pipeline within BKC
Names, Dates, Locations, Diseases, Bacteria, Proteins, …

Training Document Collection

There was an outbreak of yellow fever in Australia

Un-Tagged document

Training

There was an outbreak of <disease>yellow fever</disease> in <location>Australia</location>

Manually Tagged document

Maximize Conditional log-likelihood

$$L = \sum_{j=1}^{N} \log(P(l^j \mid o^j)) - \sum_{k} \frac{\lambda_k^2}{2\sigma^k}$$

A recent report of **mad cow disease** in **China** has authorities scrambling to deal with the issue. …

Document Collection

Labels

Y_1 — Y_2 … Y_n

X_1 X_2 … X_n

Observations

CRF Model

Tokenizer → Sentence Splitter → Part of Speech Tagger

Result Processor

A recent report of <disease>mad cow disease</disease> in <location>China<location> has authorities scrambling to deal with the issue. …

Tagged Document

14

Disease Tagging

Intuitive Representation of Disease Mode

- A **Conditional Random Field** based model allows us to utilize expert knowledge without worrying about overlapping features.

- Combines knowledge such as the following in our feature set:
  - known disease names
  - common words that end disease names
  - common orthographic endings of disease names
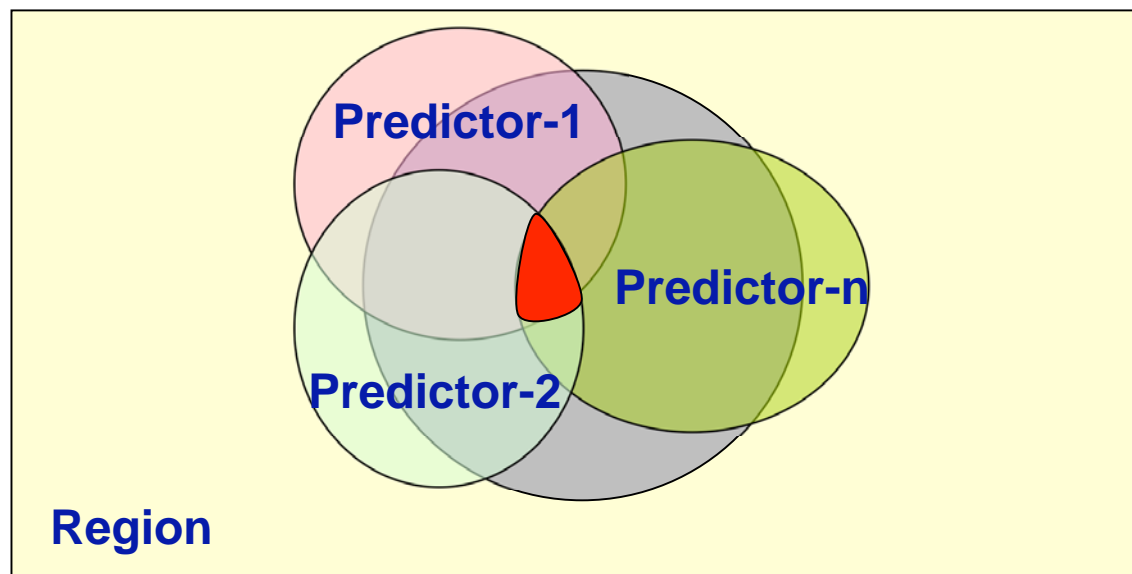 - Latin and Greek roots in words
  - parts of speech

Performance Evaluation Results

Entity	Precision	Recall	F Measure
Disease[*]	77.73	73.04	75.31
Species[¶]	94.35	92.59	93.46
Genus[¶]	92.06	87.63	89.79

[*] Training performed using 250 ProMED mail documents;

Testing performed on 100 separate ProMED mail documents.

[¶] Number of training Documents: 100 ProMED email documents

Number of testing Documents: 47 ProMED email documents

Named Entity Recognition using Meta-Learning Techniques

To make use of the *existing* tools for Named Entity Recognition by exploiting non-overlapping regions of predictions to *improve performance* for predicting Protein names.

- Region under consideration
- Protein Names under consideration
- Predictions by Predictor-1
- Predictions by Predictor-2
- Predictions by Predictor-n
- Overlapping Predictions

Meta-Learning and Weighted Voting Based Protein Named Entity Recognition

TRAINING PHASE

Training Collection

Predictor-1

Predictor-2

Predictor-n

P1	P2	P3	P4	Class
0	0	1	1	Y
1	0	1	1	Y
0	0	0	1	N

Meta – Classifier Naïve Bayes

$$P(C|P1, P2\ldots Pn) = \frac{\prod_{i=1}^{n} P(Pi|C) \cdot P(C)}{P(P1, P2, \ldots Pn)}$$

High Recall

Tagged Document

TESTING PHASE

Predictor-1

Predictor-2

Predictor-n

P1	P2	P3	P4
1	0	1	1
0	0	0	1
0	0	0	1

P1	P2	P3	P4
0	0	0	1
1	0	1	1
0	0	1	1

Combined Score

Tagged Document

Weighted Vote Selector

Tagged Document

High Precision

Document Collection

5-fold Cross-Validation Results

Pasta Data (61 Medline abstracts)

Predictor	ABNER	YAGI	KEX	LingPipe	NLProt	Voting + Meta-Classifier Score
Precision	25.9 %	33.3%	15.6 %	30.2 %	42.6 %	85.5%
Recall	58.2%	62.5 %	63.9%	73.1 %	49.9 %	67.3%

Intelligent Queries over Semantic Graphs

Processing of intelligent queries and advanced analysis of information in DHS presents a significant computational challenge.

Example Queries beyond Google

- Identify a minimum set of pathogens that are related to all the other pathogens (**Minimum Vertex Cover**);
- Discover a pattern of interest in the DB (**Sub-graph Isomorphism**);
- Find the largest group of cities so that every two cities are affected by a disease spreading from one city to another or enumerate all such groups (**Maximum or Maximal Clique**);
- Extract the maximum group of countries that have had the same disease spreading pattern this year as they had last year (**Maximum Common Subgraph**).

DHS Semantic Graph

Example: Maximum Clique

- A clique is a complete subgraph, for example, K_4:

• Finding maximum clique in a graph is *NP*-complete problem, and difficult even for small cliques on planar graphs
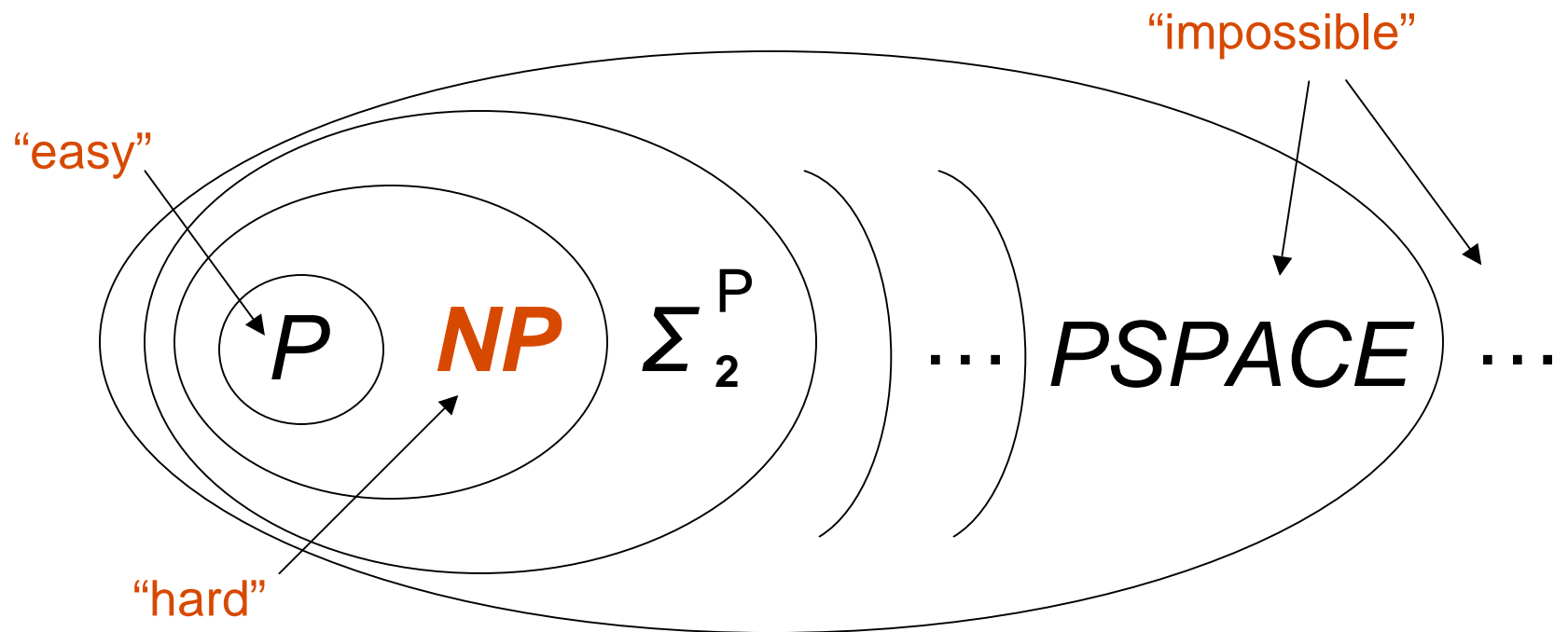
K_4

Indeed it does!

Classic Complexity Theory

- **The Classic View:**

"impossible"

"easy"

P **NP** Σ_2^P ...   *PSPACE*   ...

"hard"

Parameter Sensitivity: Instance(n,k)

- Suppose our problem is, say, *NP*-complete.

- Consider an algorithm with a time bound such as *O(2^{k+n})*.

- And now one with a time bound more like *O(2^k + n)*.

- Both are exponential in parameter value(s).

- But what happens when *k* is fixed?

Parameterized Complexity Theory

Hence, the Parameterized View:

"solvable"
(even if
NP-hard!)

"impossible"

FPT W[1] W[2] … XP …

"heuristics only"

Fixed Parameter Tractability

- Fixed Parameter Tractability offers extremely efficient methods of reducing the search space for a certain subclass of *NP*-complete problems, known as FPT.

- FPT branching techniques also offer an effective method of parallelizing difficult problems:
  - Embarrassingly parallel
  - Little or no communication between processors

- These techniques have lead to the implementation of the world's fastest codes for solving these well-known NP-complete problems.

Clique → Vertex Cover

Reduction:

- The Maximum Clique is not FPT
- Fortunately, Vertex Cover is FPT
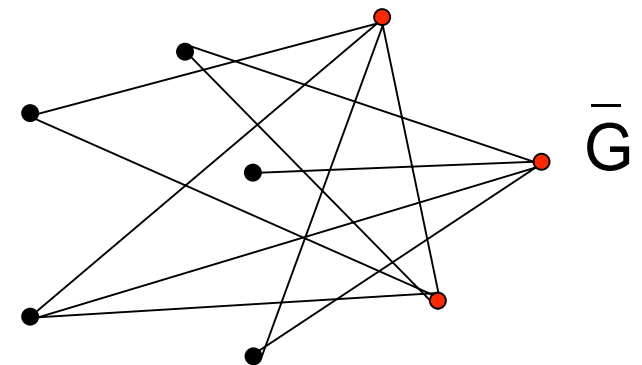- Vertex Cover is a complementary dual to Clique

Vertex Cover - Major Steps:

- **preprocess** via degree structures
- **kernelize** to computational core
- parallel **branching** explores core
- **interleave** all three

Maximum Clique (Size 5)
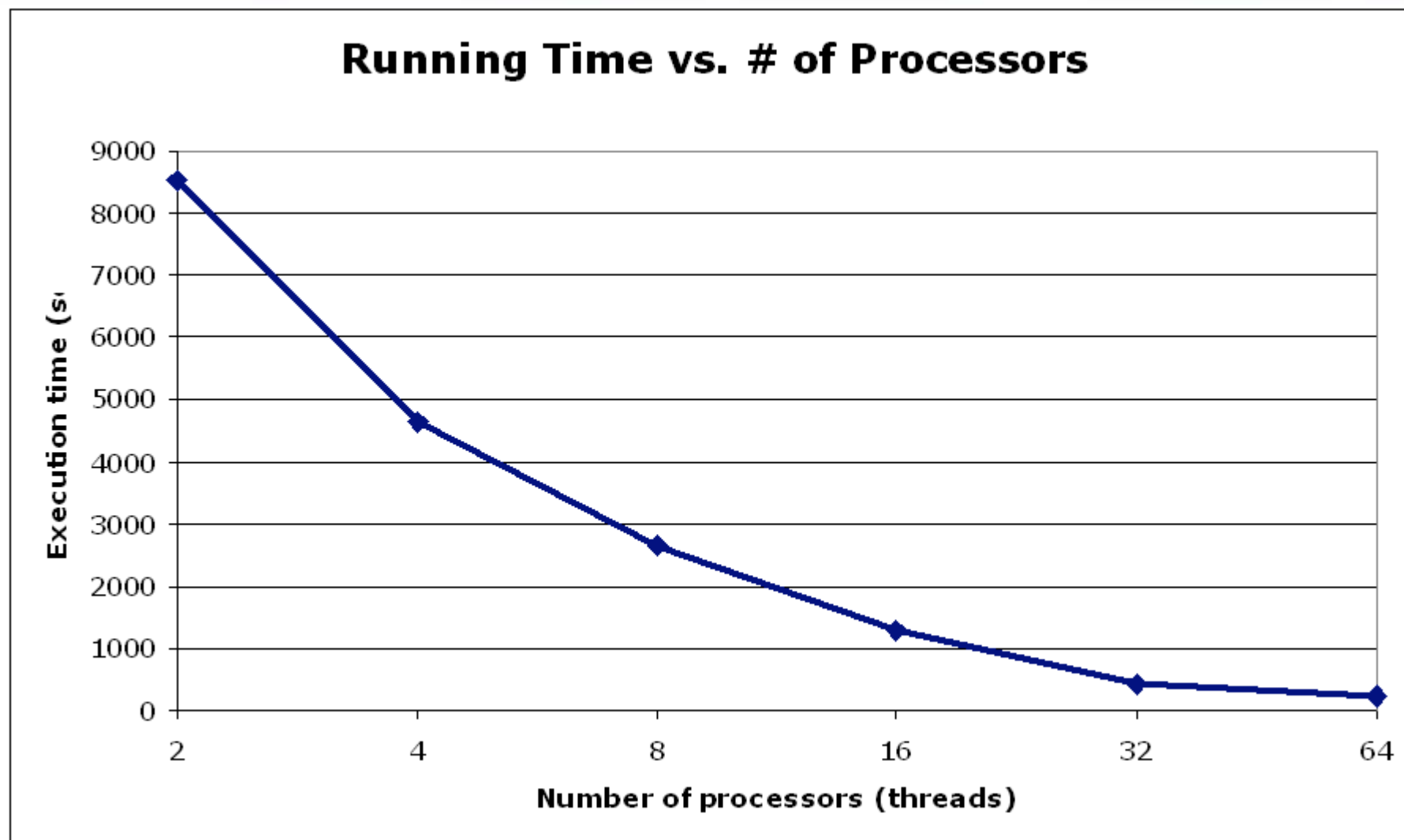

G

Minimum Vertex Cover (Size 3)

$\overline{G}$

Performance Results

Graph Name	Graph Size	Cover Size	Instance Type	Sequential Kernelization	Sequential Branching	Parallel Branching	Dynamic Decomposition
Set-1	839	399	Yes	34 seconds	7 seconds	Not needed	Not needed
Set-2	839	398	No	34 seconds	141 minutes	82 minutes	20 minutes
Set-3	2466	2044	Yes	203 minutes	~ 5 days	~ 5 days	140 minutes
Set-4	2466	2043	No	203 minutes	6+ days	6+ days	620 minutes

So clique size is 422.   A direct assault ~ 2466^{422}.
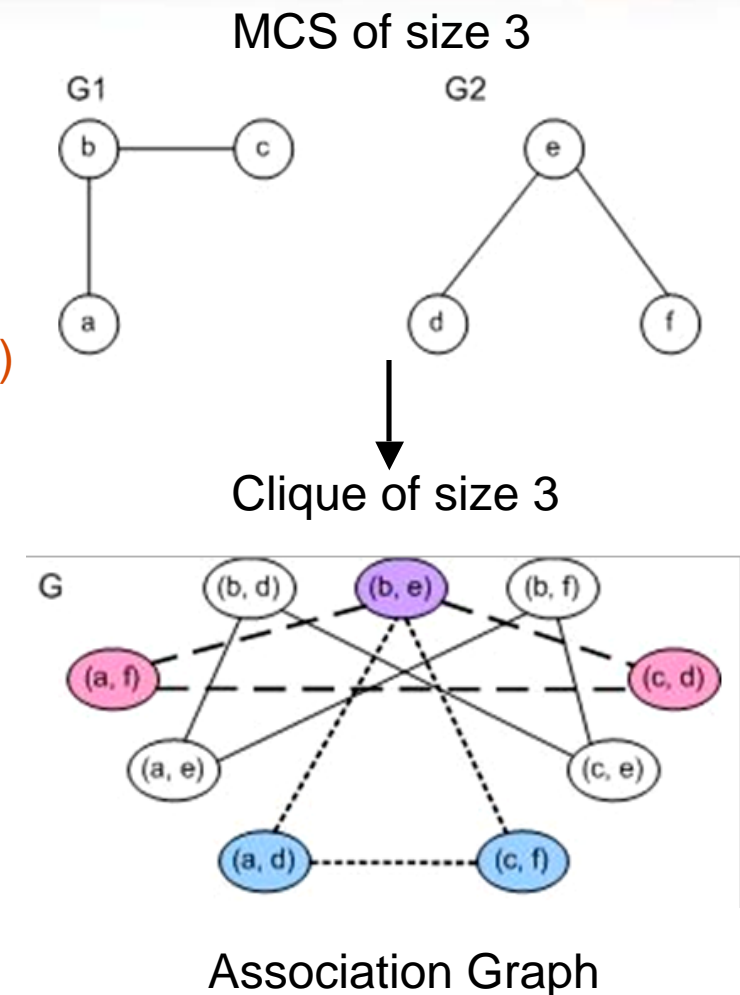
32 PEs @ 500MHz.
Load balancing is critical.
"No" is harder than "yes."

Scalability

Graph Matching → Clique

- Maximum Common Subgraph (MCS) and Subgraph Isomorphism are special cases of Graph Matching.

- Existing approaches to MCS:
  - Clique-based (Bron-Kerbosch, Robson); $O(1.19^{mn})$
  - Backtracking (McGregor, Krissinel); $O(m^{n+1}n)$
  - Dynamic programming (Akutsu) (trees of bounded degree)

- MCS is not FPT. But we solve MCS by reducing it to Clique on the *association graph*.

- Our method is the fastest known on general graphs with $O((m+1)^n)$ but much better in practice since there are much less choices for branching than (m+1)

MCS of size 3

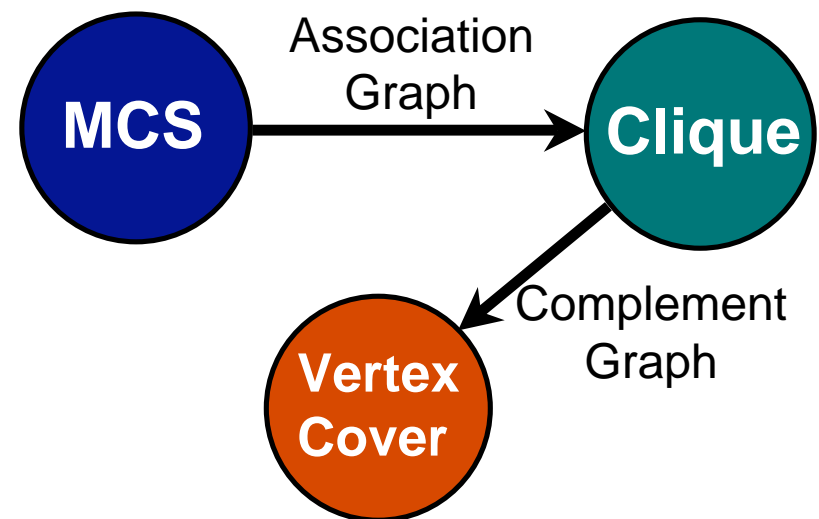Clique of size 3

Association Graph

Scalable Algorithms for Semantic Graphs

Prototyped a library of scalable parallel graph matching algorithms for NP-hard graph problems with polynomial time solution.

Library Features:

- **Exact polynomial** solutions via **Fixed Parameter Tractability** (FPT) reduction:
  - Minimum Vertex Cover (VC)
  - Sub-graph Isomorphism (SI)
  - Maximum or Maximal Clique (Clique)
  - Maximum Common Subgraph (MCS)

- The **fastest and most scalable** (in problem size) than reported in literature.

- Supports different types of graphs: directed, undirected, labeled, and unlabeled.

MCS → (Association Graph) → Clique → (Complement Graph) → Vertex Cover

Example Semantic Graph:
12,422 vertices and >100M edges
Maximum Clique: 399 vertices

Summary

***Goal**: Provide a capability for automated mapping of unstructured free text to Semantic Graph and for efficient query over Semantic Graph.*

- **Motivation**
  - The construction of the concept graphs from unstructured text is a very labor intensive and tedious task that requires automation.
  - Semantic graph queries are often NP-complete
- **Major accomplishments**
  - Intelligent text preprocessing
  - Advanced methods for concepts extraction, scoring, and mapping
  - Scalable graph algorithms over semantic graphs
- **Benefits**
  - Facilitate free text data feed to the BKC semantic graph.
  - Discover advanced knowledge from the semantic graph.